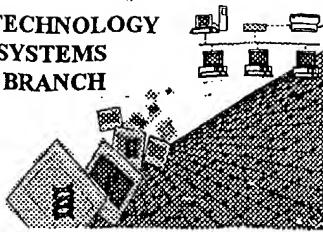# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/713,006_

Source: _TWO_

Date Processed by STIC: _12/2/03_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
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2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 4.1 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
<u>http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm</u>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
<u>Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:</u>

1. EFS-Bio (<u><http://www.uspto.gov/ebc/efs/downloads/documents.htm></u> , **EFS Submission User Manual** - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (**EFFECTIVE 12/01/03**):
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

IFWO

RAW SEQUENCE LISTING   DATE: 12/02/2003
PATENT APPLICATION: US/10/713,006   TIME: 15:21:36

Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\12022003\J713006.raw

```
 3 <110> APPLICANT: PROTEUS S.A.
 4       DUPRET, Daniel
 5       LEFEVRE, Fabrice
 6       FOURAGE, Laurent
 8 <120> TITLE OF INVENTION: METHOD OF PREPARING POLYNUCLEOTIDE FRAGMENTS FOR USE
 9       IN SHUFFLING, AND SHUFFLING OF SAME
W--> 10 <130> FILE REFERENCE: 26883PCT-PP15
W--> 11 <140> CURRENT APPLICATION NUMBER: PCT/IB02/02769
C--> 12 <141> CURRENT FILING DATE: 2003-11-17
W--> 13 <160> NUMBER OF SEQ ID: 2
     14 <170> SOFTWARE: PatentIn version 3.1
```

ERRORED SEQUENCES

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W--> 15 <210> SEQ ID NO: 1
     16 <211> LENGTH: 27
     17 <212> TYPE: DNA
     18 <213> ORGANISM: Artificial
     20 <220> FEATURE:
W--> 21 <221> NAME/KEY: primer
     22 <222> LOCATION: (1)..(27)
     23 <223> OTHER INFORMATION: sense primer pET5'
W--> 24 <400> SEQUENCE: 1
E--> 25 agatctcgat cccgcgaaat taatacg
     26 <210> SEQ ID NO: 2
     27 <211> LENGTH: 26
     28 <212> TYPE: DNA
     29 <213> ORGANISM: artificial
     31 <220> FEATURE:
W--> 32 <221> NAME/KEY: primer
     33 <222> LOCATION: (1)..(26)
     34 <223> OTHER INFORMATION: antisense primer pET3'
W--> 35 <400> SEQUENCE: 2
E--> 36 agatctcgat cccgcgaaat taatacg
W--> 38 ATTENTION: Please note that this document was reconstructed to
W--> 39 correct inherent conversion issues. Great care has been taken to ensure
W--> 40 that all formatting unique to this document was preserved.  Nonetheless,
W--> 41 you should review all document formats.  If this document had automatic
W--> 42 numbering, the numbering has been hard coded to text.  To re-establish
W--> 43 automatic numbering, you MUST reapply it and, if required, reinsert the
W--> 44 Table of Contents.  Use the DocXtools toolbar and select DocXNumbering,
W--> 45 then Automation for Softwise Numbering Suite, to assist you with
```

[Handwritten annotations: "Does Not Comply Corrected Diskette Needed (P.1)"; "please insert Number OF Nucleotide bases" (arrow pointing to line 25); "26 → 27" (next to line 27 LENGTH); "same error" (arrow pointing to line 36); "delete" (bracketing lines 38–45)]

RAW SEQUENCE LISTING   DATE: 12/02/2003
PATENT APPLICATION: **US/10/713,006**   TIME: 15:21:36

Input Set : **A:\PTO.KD.txt**
Output Set: **N:\CRF4\12022003\J713006.raw**

```
W--> 46  reinserting automatic numbering.  Contact the Information Center should
W--> 47  you have any further questions.  *Upon completion of your review, please
E--> 48  delete this comment. Thank you.*
```

delete

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 12/02/2003
PATENT APPLICATION: **US/10/713,006**   TIME: 15:21:37

Input Set : **A:\PTO.KD.txt**
Output Set: **N:\CRF4\12022003\J713006.raw**

<u>Invalid <213> Response:</u>
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2

VERIFICATION SUMMARY   DATE: 12/02/2003
PATENT APPLICATION: **US/10/713,006**   TIME: 15:21:37

Input Set : **A:\PTO.KD.txt**
Output Set: **N:\CRF4\12022003\J713006.raw**

```
L:10 M:283 W: Missing Blank Line separator, <130> field identifier
L:11 M:283 W: Missing Blank Line separator, <140> field identifier
L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:13 M:283 W: Missing Blank Line separator, <160> field identifier
L:15 M:283 W: Missing Blank Line separator, <210> field identifier
L:21 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:24 M:283 W: Missing Blank Line separator, <400> field identifier
L:25 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:27 SEQ:1
L:32 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:35 M:283 W: Missing Blank Line separator, <400> field identifier
L:36 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:27 SEQ:2
L:38 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:9
L:39 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:39 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:11
L:40 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:40 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:10
L:41 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:41 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:11
L:42 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:42 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:11
L:43 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:43 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:11
L:44 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:44 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:10
L:45 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:45 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:10
L:46 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:46 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:8
L:47 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:47 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:10
L:48 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:48 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:5
L:48 M:252 E: No. of Seq. differs, <211> LENGTH:Input:26 Found:27 SEQ:2
```